

# WEST Search History

[Hide Items](#)[Restore](#)[Clear](#)[Cancel](#)

DATE: Monday, November 07, 2005

<b>Hide?</b>	<b>Set Name</b>	<b>Query</b>	<b>Hit Count</b>
		<i>DB=USPT,PGPB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L16	("ISH-HOROWICZ-DAVID".IN.)!	7
		<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L15	l14 and @ay<1999	17
<input type="checkbox"/>	L14	L13 and l11	113
<input type="checkbox"/>	L13	delta\$2 adj8 antibod\$4	524
<input type="checkbox"/>	L12	delta\$2 8adj antibod\$4	0
<input type="checkbox"/>	L11	L10 and antibod\$	5458
<input type="checkbox"/>	L10	L9 and (bertebrate or mammal\$3 or human)	6202
<input type="checkbox"/>	L9	L6 and ((tyrosine kinase) or jagged or dsl)	6282
<input type="checkbox"/>	L8	L7 and antibod\$	16279
<input type="checkbox"/>	L7	L6 and (vertebrate or mammal\$3 or human)	20893
<input type="checkbox"/>	L6	Delta\$2 and (notch or kinase)	28615
<input type="checkbox"/>	L5	Delta and (notch or kinase)	24202
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	6121045.pn.	1
<input type="checkbox"/>	L3	6337387.pn.	1
<input type="checkbox"/>	L2	6262025.pn.	1
<input type="checkbox"/>	L1	5834208.pn.	1

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 13:00:13 ON 07 NOV 2005)

FILE 'MEDLINE' ENTERED AT 13:00:28 ON 07 NOV 2005

E SAKANO S/AU

L1 60 S E3-E4

L2 9 S L1 AND KINASE

FILE 'STNGUIDE' ENTERED AT 13:01:56 ON 07 NOV 2005

FILE 'GENBANK' ENTERED AT 13:02:40 ON 07 NOV 2005

SET NOTICE DISPLAY 1

SET NOTICE LOGIN DISPLAY

FILE 'MEDLINE' ENTERED AT 13:04:09 ON 07 NOV 2005

=>

STIC-Biotech/ChemLib

170868

From: Chan, Christina  
Sent: Monday, November 07, 2005 2:55 PM  
To: Kaufman, Claire; STIC-Biotech/ChemLib  
Subject: RE: rush sequence search 09/783931

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
NOV - 7 2005  
STIC/CHL DIVISION  
(STIC)

-----Original Message-----

From: Kaufman, Claire  
Sent: Monday, November 07, 2005 12:24 PM  
To: Chan, Christina  
Subject: FW: rush sequence search 09/783931

Christina, I need a rush sequence search for a due an after final that is allowable. Please forward this request to STIC. Thanks, Claire

-----  
RUSH \*\*\*\*\* RUSH \*\*\*\*\* RUSH \*\*\*\*\* RUSH\*\*\*

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70  
Room:Rem 4E85 Serial #:09/783,931 Date:11/07/05

Please search nucleic acid sequences SEQ ID NO:24 in interference databases only.

Please show top 30 hits.

Please put results on disk.

Thanks,  
Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

4C70

\*\*\*\*\*

Searcher: Jan  
Searcher Phone: 22504  
Date Searcher Picked up: 11/8  
Date completed: 11/14  
Searcher Prep Time: 10  
Online Time: 26

\*\*\*\*\*

Type of Search  
NA# ✓ AA#:         
S/L:        Oligomer:         
Encode/Transl:         
Structure #:        Text:         
Inventor:        Litigation:       

\*\*\*\*\*

Vendors and cost where applicable  
STN:         
DIALOG:         
QUESTEL/ORBIT:         
LEXIS/NEXIS:         
SEQUENCE SYSTEM: ✓  
WWW/Internet:         
Other (Specify):

159298

STIC-Biotech/ChemLib

From: Kaufman, Claire  
Sent: Thursday, July 14, 2005 12:21 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 09/783931

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70  
Room:Rem 4E85 Serial #:09/783931 Date:7/14/05

-----  
Please search SEQ ID NO:23 in commercial databases.

Please put results on disk.

Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

\*\*\*\*\*

STAFF USE ONLY

Searcher:\_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up:\_\_\_\_\_  
Date Completed:\_\_\_\_\_  
Searcher Prep/Rev. Time:\_\_\_\_\_  
Online Time:\_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#:\_\_\_\_ AA#:\_\_\_\_\_  
Interference:\_\_\_\_ SPDI:\_\_\_\_\_  
S/L:\_\_\_\_ Oligomer:\_\_\_\_\_  
Encode/Transl:\_\_\_\_\_  
Structure#:\_\_\_\_ Text:\_\_\_\_\_  
Inventor:\_\_\_\_ Litigation:\_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN:\_\_\_\_\_  
DIALOG:\_\_\_\_\_  
QUESTEL/ORBIT:\_\_\_\_\_  
LEXIS/NEXIS:\_\_\_\_\_  
SEQUENCE SYSTEM:\_\_\_\_\_  
WWW/Internet:\_\_\_\_\_  
Other(Specify):\_\_\_\_\_

STIC-Biotech/ChemLib

158956

From: Kaufman, Claire  
Sent: Tuesday, July 12, 2005 9:29 AM  
To: STIC-Biotech/ChemLib  
Subject: FW: rush sequence search 09/783931

-----Original Message-----

From: Low, Christopher  
Sent: Monday, July 11, 2005 4:53 PM  
To: Kaufman, Claire  
Subject: RE: rush sequence search 09/783931

approved

Christopher Low  
SPE 1614 / TCAR 1600  
REM 3E88 / (571) 272-0951

-----Original Message-----

From: Kaufman, Claire  
Sent: Monday, July 11, 2005 02:51 PM  
To: Low, Christopher  
Subject: rush sequence search 09/783931

Chris, I need a rush sequence search for a due amended that is allowable (much to my surprise). Please forward this request to STIC. Thanks, Claire

-----  
RUSH \*\*\*\*\* RUSH \*\*\*\*\* RUSH \*\*\*\*\* RUSH\*\*\*

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70  
Room: Rem 4E85 Serial #: 09/783,931 Date: 7/11/05

-----  
Please search nucleic acid sequences SEQ ID NO: 1, 11, 14 and 26  
and protein sequences SEQ ID NO: 2, 12 and 65 in interference databases only.

For nucleic acid sequences, please list top 30 hits.

Please put results on disk.

Thanks,  
Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

\*\*\*\*\*

STAFF USE ONLY

Searcher: D. S. Chivers  
Searcher Phone: 2- 2526  
Date Searcher Picked up: 7/18  
Date Completed: 7/18  
Searcher Prep/Rev. Time: 23  
Online Time: 8

\*\*\*\*\*

Type of Search

NA#: 4 AA#: 3  
Interference: ✓ SPDI:         
S/L:        Oligomer:         
Encode/Transl:         
Structure#:        Text:         
Inventor:        Litigation:       

\*\*\*\*\*

Vendors and cost where applicable

STN:         
DIALOG:         
QUESTEL/ORBIT:         
LEXIS/NEXIS:         
SEQUENCE SYSTEM: Comp 454  
WWW/Internet:         
Other(Specify):

STIC-Biotech/ChemLib

138232

mej

From: Kaufman, Claire  
Sent: Thursday, November 18, 2004 1:57 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence 09/783,931

RECEIVED  
NOV 18 2004  
TECH/CHEM. Division  
(STIC)

## SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70  
Room:Rem 4E85 Serial #:09/783,931 Date:11/18/04

Please search SEQ ID NO:65 and the fragment of SEQ ID NO:26 from 60-665 in interference databases only.

Please put results on paper.

Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

\*\*\*\*\*

### STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

### Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

### Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

OM nucleic - nucleic search, using sw model

Run on: November 14, 2005, 05:15:01 ; Search time 490 Seconds  
(without alignments)  
9680.747 Million cell updates/sec

Title: US-09-783-931B-24  
Perfect score: 2899  
Sequence: 1 gtccagcggtaccatgggcc.....aataaatataatgaactaca 2899

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	2742.8	94.6	2899	3	US-08-981-392-24	Sequence 24, Appl	
2	2742.8	94.6	2899	4	US-09-908-322-24	Sequence 24, Appl	
3	2371.2	81.8	2857	3	US-08-981-392-4	Sequence 4, Appli	
4	2371.2	81.8	2857	4	US-09-908-322-4	Sequence 4, Appli	
5	2133.4	73.6	2692	3	US-08-981-392-11	Sequence 11, Appl	
6	2133.4	73.6	2692	4	US-09-908-322-11	Sequence 11, Appl	
7	1780	61.4	1981	3	US-08-981-392-26	Sequence 26, Appl	
8	1780	61.4	1981				

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OM nucleic - nucleic search, using sw model

Run on: November 14, 2005, 05:24:01 ; Search time 2032 Seconds  
(without alignments)  
11798.330 Million cell updates/sec

Title: US-09-783-931B-24  
Perfect score: 2899  
Sequence: 1 gtccagcgggtaccatgggcc.....aataaatataatgaactaca 2899

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq2:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 27: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*



28: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2742.8	94.6	2899	9	US-09-908-322-24		Sequence 24, Appl
2	2742.8	94.6	2899	10	US-09-783-931-24		Sequence 24, Appl
3	2409.6	83.1	2857	20	US-10-731-741-9		Sequence 9, Appli
4	2409.6	83.1	2857				

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 410.08 Seconds  
 (without alignments)  
 10007.261 Million cell updates/sec

Title: US-09-783-931A-1  
 Perfect score: 2508  
 Sequence: 1 gaattcggcagcagggttttt.....tcgataccggtcatcaagctt 2508

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2508	100.0	2508	3	US-08-981-392-1	Sequence 1, Appli
2	2508	100.0	2508	4	US-09-908-322-1	Sequence 1, Appli
3	2460.6	98.1	2883	3	US-08-981-392-3	Sequence 3, Appli
4	2460.6	98.1	2883	4	US-09-908-322-3	Sequence 3, Appli
5	1442.4	57.5	2663	3	US-09-068-740A-8	Sequence 8, Appli
6	1442.4	57.5	2663	4	US	

OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 1545.61 Seconds  
(without alignments)  
10210.150 Million cell updates/sec

Title: US-09-783-931A-1  
Perfect score: 2508  
Sequence: 1 gaattcgggcacgaggtttttt.....tcgataccgtcatcaagctt 2508

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2508	100.0	2508	9	US-09-908-322-1		Sequence 1, Appli
2	2508	100.0	2508	10	US-09-783-931-1		Sequence 1, Appli
3	2460.6	98.1	2883	9	US-09-908-322-3		Sequence 3, Appli
4	2460.6	98.1	2883	10	US-09-783-931-3		Sequence 3, Appli
5	2458.6	98.0	2883	20	US-10-877-563-10		Sequence 10, Appl
6	1891.8	75.4	2088	20	US-10-877-563-9		Sequence 9, Appli
7	1442.4	57.5					

OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:13:45 ; Search time 9833.79 Seconds  
 (without alignments)  
 10411.464 Million cell updates/sec

Title: US-09-783-931A-1  
 Perfect score: 2508  
 Sequence: 1 gaattcggcagcagggttttt.....tcgataccggtcatcaagctt 2508

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*  
 1: /cgn2\_6/ptodata/1/pna/PCTUS1\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/pna/PCTUS2\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq:\*  
 4: /cgn2\_ /1/pna/US6058\_COMB.seq:\*  
 129: /cgn2\_6/ptodata/1/pna/US6059\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%				
No.	Score	Query	Match	Length	ID	Description
1	2508	100.0	2508	34	US-09-783-931-1	Sequence 1, Appli
2	2460.6	98.1	2883	34	US-09-783-931-3	Sequence 3, Appli
3	2458.6	98.0	2883	20	US-09-310-685-10	Sequence 10, Appl
4	2458.6	98.0	2883	64	US-10-877-563-10	Sequence 10, Appl
5	2458.6	98.0	2883	68	US-11-022-478-10	Sequence 10, Appl
6	1891.8	75.4	2088	20	US-09-310-685-9	Sequence 9, Appli
7	1891.8	75.4	2088	64	US-10-877-563-9	Sequence 9, Appli
8	1891.8	75.4				

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 440.166 Seconds  
(without alignments)  
10007.261 Million cell updates/sec

Title: US-09-783-931A-11  
Perfect score: 2692  
Sequence: 1 ctgcaggaattcsmycgcat.....gctcccaacgcgttggaggt 2692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2690.8	100.0	2692	3	US-08-981-392-11		Sequence 11, Appl
2	2690.8	100.0	2692	4	US-09-908-322-11		Sequence 11, Appl
3	2506.6	93.1	2857	3	US-08-981-392-4		Sequence 4, Appli
4	2506.6	93.1	2857	4	US-09-908-322-4		Sequence 4, Appli
5	2133.4	79.2	2899	3	US-08-981-392-24		Sequence 24, Appl
6	2133.4	79.2	2899	4	US-09-908-322-24		Sequence 24, Appl
7	1679.8	62.4	2663	3	US-09-		

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 1659.01 Seconds  
(without alignments)  
10210.150 Million cell updates/sec

Title: US-09-783-931A-11  
Perfect score: 2692  
Sequence: 1 ctgcaggaattcsmycgcat.....gctcccaacgcgttgaggt 2692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2690.8	100.0	2692	9	US-09-908-322-11	Sequence 11, Appl
2	2690.8	100.0	2692	10	US-09-783-931-11	Sequence 11, Appl
3	2666.2	99.0	2692	20	US-10-877-563-13	Sequence 13, Appl
4	2577.8	95.8	2857	19	US-10-731-741-9	Sequence 9, Appli
5	2577.8	95.8	2857	21	US-10-764-420-2345	Sequence 2345, Ap
6	2506.6	93.1	2857	9	US-09-908-322-4	Sequence 4, Appli
7	2506.6	93.1	2857	10	US-09-783-931-4	Sequence 4, Appli
8	2133.4	79.2	2899	9	US-09-908-322-	

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:13:45 ; Search time 10555.3 Seconds  
(without alignments)  
10411.464 Million cell updates/sec

Title: US-09-783-931A-11  
Perfect score: 2692  
Sequence: 1 ctgcaggaattcsmycgcat.....gctcccaacgcgttgaggt 2692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*  
1: /cgn2\_6/ptodata/1/pna/PCTUS1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/PCTUS2\_COMB.seq:\*  
3: /.seq:\*  
129: /cgn2\_6/ptodata/1/pna/US6059\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2690.8	100.0	2692	34	US-09-783-931-11	Sequence 11, Appl	
2	2666.2	99.0	2692	20	US-09-310-685-13	Sequence 13, Appl	
3	2666.2	99.0	2692	64	US-10-877-563-13	Sequence 13, Appl	
4	2666.2	99.0	2692	68	US-11-022-478-13	Sequence 13, Appl	
5	2582.6	95.9	2857	48	US-10-144-771-1551	Sequence 1551, Ap	
6	2582.6	95.9	2857	106	US-60-360-207-1551	Sequence 1551, Ap	
7	2577.8	95.8	2857	62	US-10-731-741-9	Sequence 9, Appli	
8	2577.8	95.8	2857	62	US-10-764-420-2345	Sequence 2345, Ap	
9	2506.6	93.1	2857	34	US-09-783-931-4	Sequence 4, Appli	
10	2436.8	90.5	2988	65	US-10-913-487-12	Sequence 12, Appl	
11	2133.4	79.2	2899	34	US-09-783-931-24	Sequence 24, Appl	
12	2123.8	78.9	2795	2	PCT-US03-03482-3930	Sequence 3930, Ap	
13	2123.8	78.9	2795	53	US-10-357-507-3930	Sequence 3930, Ap	
14	1982.8	73.7	2926	65	US-10-913-487-13	Sequence 13, Appl	



OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 70.7929 Seconds  
 (without alignments)  
 761.328 Million cell updates/sec

Title: US-09-783-931A-12  
 Perfect score: 4121  
 Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	4121	100.0		722	3	US-08-981-392-12	Sequence 12, Appl
2	4121	100.0		722	4	US-09-908-322-12	Sequence 12, Appl
3	3971	96.4		720	3	US-08-872-855-4	Sequence 4, Appli
4	3840.5	93.2		713	3	US-08-872-855-5	Sequence 5, Appli
5	3659.5	88.8		723	3	US-09-068-740A-9	Sequence 9, Appli
6	3659.5	88.8		723	4	US-09-423-753-27	Sequence 27, Appl
7	3631.5	88.1		723	4	US-09-641-612-6	Sequence 6, Appli
8	3571.5	86.7		702	3	US-09-068-740A-4	Sequence 4, Appli
9	3368	81.7		728	3	US-08-981-392-2	Sequence 2, Appli
10	3368	81.7		728	4	US-09-908-322-2	Sequence 2, Appli
11							

OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 247.116 Seconds  
 (without alignments)  
 1130.390 Million cell updates/sec

Title: US-09-783-931A-12  
 Perfect score: 4121  
 Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
 3: /cgn2\_6/  
 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4121	100.0	722	9	US-09-908-322-12	Sequence 12, Appl
2	4121	100.0	722	10	US-09-783-931-12	Sequence 12, Appl
3	4007	97.2	722	16	US-10-877-563-14	Sequence 14, Appl
4	4003	97.1	722	15	US-10-042-865-107	Sequence 107, App
5	4003	97.1	722	16	US-10-731-741-4	Sequence 4, Appli
6	3971	96.4	720	14	US-10-417-719-4	Sequence 4, Appli
7	3848	93.4	714	15	US-10-042-865-108	Sequence 108, App
8	3840.5	93.2	713	14	US-10-417-719-5	Sequence 5, Appli
9	3659.5	88.8	723	9	US-09-828-366-21	Sequence 21, Appl
10	3659.5	88.8	723	9	US-09-995-593A-9	Sequence 9, Appli
11	3659.5	88.8	723	14	US-10-028-072-346	Sequence 346, App

OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 85.8422 Seconds  
(without alignments)  
10007.261 Million cell updates/sec

Title: US-09-783-931A-14  
Perfect score: 525  
Sequence: 1 tacgatgaayaacctggcgga.....aggacgagtgcgatcatcgca 525

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	521.4	99.3	525	3	US-08-981-392-14	Sequence 14, Appl
2	521.4	99.3	525	4	US-09-908-322-14	Sequence 14, Appl
3	188.6	35.9	2183	4	US-09-641-612-9	Sequence 9, Appli
4	188.6	35.9	2663	3	US-09-068-740A-8	Sequence 8, Appli
5	188.6	35.9	2663	4	US-09-423-753-8	Sequence 8, Appli
6	174.8	33.3	1981	3	US-08-981-392-26	Sequence 26, Appl
7	174.8	33.3	1981	4	US-09-908-322-26	Sequence 26, Appl
8	159.6	30.4	2899	3	US-08-981-392-24	Sequence 24, Appl
9	159.6	30.4	2899	4	US-09-908-322-24	

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 323.543 Seconds  
(without alignments)  
10210.150 Million cell updates/sec

Title: US-09-783-931A-14  
Perfect score: 525  
Sequence: 1 tacgatgaayaacctggcgca.....aggacgagtgcgtcatcgca 525

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	521.4	99.3	525	9	US-09-908-322-14	Sequence 14, Appl
2	521.4	99.3	525	10	US-09-783-931-14	Sequence 14, Appl
3	519.4	98.9	525	20	US-10-877-563-15	Sequence 15, Appl
4	282.4	53.8	468	10	US-09-918-995-29101	Sequence 29101, A
5	188.6	35.9	2183	19	US-10-644-548-9	Sequence 9, Appli
6	188.6	35.9	2663	9	US-09-995-593A-8	Sequence 8, Appli
7	188.6	35.9	2663	14	US-10-241-476-8	Sequence 8, Appli
8	188.6	35.9	2663	24	US-11-051-618B-8	Sequence 8, Appli
9	188.6	35.9	2663	24	US-11-051-631-8	Sequence 8, Appli
10	188.6	35.9	2933	9	US-09-828-366-20	Sequence 20, Appl
11	188.6	35.9	2933	14	US-10-028-072-345	

OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 71.3812 Seconds  
(without alignments)  
761.328 Million cell updates/sec

Title: US-09-783-931A-2  
Perfect score: 4153  
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIIATEV 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4153	100.0	728	3	US-08-981-392-2	Sequence 2, Appli
2	4153	100.0	728	4	US-09-908-322-2	Sequence 2, Appli
3	4142.5	99.7	729	3	US-08-872-855-8	Sequence 8, Appli
4	3495.5	84.2	721	3	US-08-981-392-5	Sequence 5, Appli
5	3495.5	84.2	721	4	US-09-908-322-5	Sequence 5, Appli
6	3494.5	84.1	723	3	US-09-068-740A-9	Sequence 9, Appli
7	3494.5	84.1	723	4	US-09-423-753-27	Sequence 27, Appli
8	3491.5	84.1	721	3	US-08-872-855-7	Sequence 7, Appli
9	3466.5	83.5	723	4	US-09-641-612-6	

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OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 249.169 Seconds  
(without alignments)  
1130.390 Million cell updates/sec

Title: US-09-783-931A-2  
Perfect score: 4153  
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIIATEV 728

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4153	100.0	728	9	US-09-908-322-2	Sequence 2, Appli
2	4153	100.0	728	10	US-09-783-931-2	Sequence 2, Appli
3	4142.5	99.7	729	14	US-10-417-719-8	Sequence 8, Appli
4	4135	99.6	728	16	US-10-877-563-11	Sequence 11, Appl
5	3495.5	84.2	721	9	US-09-908-322-5	Sequence 5, Appli
6	3495.5	84.2	721	10	US-09-783-931-5	Sequence 5, Appli
7	3495.5	84.2	721	15	US-10-042-865-109	Sequence 109, App
8	3494.5	84.1	723	9	US-09-828-366-21	Sequence 21, Appl
9	3494.5	84.1	723	9	US-09-995-593A-9	Sequence 9, Appli

OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 323.911 Seconds  
 (without alignments)  
 10007.261 Million cell updates/sec

Title: US-09-783-931A-26  
 Perfect score: 1981  
 Sequence: 1 cattgggtacgggccccct.....attccgntttcaaagttttt 1981

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1956	98.7	1981	3	US-08-981-392-26	Sequence 26, Appl
2	1956	98.7	1981	4	US-09-908-322-26	Sequence 26, Appl
3	1780	89.9	2899	3	US-08-981-392-24	Sequence 24, Appl
4	1780	89.9	2899	4	US-09-908-322-24	Sequence 24, Appl
5	1526.2	77.0	2663	3	US-09-068-740A-8	Sequence 8, Appli
6	1526.2	77.0	2663	4	US-09-423-753-8	Sequence 8, Appli
7	1524.6	77.0	2183	4	US-09-641-612-9	Sequence 9, Appli
8	1134.2	57.3	2692	3	US-08-981-392-11	Sequence 11, Appl
9	1134.2	57.3	2692	4	US-09-908-	

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 1220.84 Seconds  
(without alignments)  
10210.150 Million cell updates/sec

Title: US-09-783-931A-26  
Perfect score: 1981  
Sequence: 1 cattgggtacgggccccct.....attccgntttcaaagttttt 1981

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1956	98.7	1981	9	US-09-908-322-26	Sequence 26, Appl	
2	1956	98.7	1981	10	US-09-783-931-26	Sequence 26, Appl	
3	1943.8	98.1	1981	20	US-10-877-563-16	Sequence 16, Appl	
4	1780	89.9	2899	9	US-09-908-322-24	Sequence 24, Appl	
5	1780	89.9	2899	10	US-09-783-931-24	Sequence 24, Appl	
6	1526.2	77.0	2663	9	US-09-995-593A-8	Sequence 8, Appli	
7	1526.2	77.0	2663	14	US-10-241-476-8	Sequence 8, Appli	
8	1526.2	77.0	2663	24	US-11-051-618B-8	Sequence 8, Appli	
9	1526.2	77.0	2663	24	US-11-051-631-8	Sequence 8, Appli	
10	1526.2	77.0	2933	9	US-09-828-366-20	Sequence 20, Appl	
11	1526.2	77.0	2933	14	US-10-028-072-345	Sequence	



OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 18.8258 Seconds  
(without alignments)  
761.328 Million cell updates/sec

Title: US-09-783-931A-65  
Perfect score: 1160  
Sequence: 1 GFTWPGTFSLIIEALHTDSP.....CNQDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	1160	100.0	192	3	US-08-981-392-65	Sequence 65, Appl	
2	1160	100.0	192	4	US-09-908-322-65	Sequence 65, Appl	
3	1160	100.0	276	3	US-08-981-392-43	Sequence 43, Appl	
4	1160	100.0	276	4	US-09-908-322-43	Sequence 43, Appl	
5	1160	100.0	520	3	US-09-068-740A-3	Sequence 3, Appli	
6	1160	100.0	702	3	US-09-068-740A-4	Sequence 4, Appli	
7	1160	100.0	723	3	US-09-068-740A-9	Sequence 9, Appli	
8	1160	100.0	723	4	US-09-423-753-27	Sequence 27, Appl	
9	1153	99.4	723	4	US-09-641-612-6	Sequence 6, Appli	
10	1138	98.1	728	3	US-08-981-392-2	Sequence 2, Appli	
11	1138	98.1	728	4	US-09-908-322-2		

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OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 65.715 Seconds  
(without alignments)  
1130.390 Million cell updates/sec

Title: US-09-783-931A-65  
Perfect score: 1160  
Sequence: 1 GFTWPGTFSLIIEALHTDSP.....CNQDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3:  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1160	100.0	192	9	US-09-908-322-65	Sequence 65, Appl
2	1160	100.0	192	10	US-09-783-931-65	Sequence 65, Appl
3	1160	100.0	192	16	US-10-877-563-17	Sequence 17, Appl
4	1160	100.0	276	9	US-09-908-322-43	Sequence 43, Appl
5	1160	100.0	276	10	US-09-783-931-43	Sequence 43, Appl
6	1160	100.0	331	17	US-10-846-989-24	Sequence 24, Appl
7	1160	100.0	331	18	US-10-845-834A-24	Sequence 24, Appl
8	1160	100.0	369	17	US-10-846-989-29	Sequence 29, Appl
9	1160	100.0	369	18	US-10-845-834A-29	Sequence 29, Appl
10	1160	100.0	484	17	US-10-846-989-34	Sequence 34, Appl
11	1160	100.0	484	18	US-10-845-834A-34	Sequence 34, Appl
12	1160	100.0	520	9	US-09-995-593A-3	Sequence 3, Appli



OM protein - protein search, using sw model

Run on: July 15, 2005, 14:49:23 ; Search time 165 Seconds  
(without alignments)  
410.200 Million cell updates/sec

Title: US-09-783-931A-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	908	98.1	175	2	AAW11724	Aaw11724 H-Delta-1
2	678.5	73.3	175	2	AAW11721	Aaw11721 H-Delta-1
3	527.5	57.0	702	2	AAW18349	Aaw18349 Prolifera
4	527.5	57.0	702	2	AAW75495	Aaw75495 Truncated
5	527.5	57.0	723	2	AAW18353	Aaw18353 Prolifera
6	527.5	57.0	723	2	AAW75492	Aaw75492 Human del
7	527.5	57.0	723	2	AAW94498	Aaw94498 Human del
8	527.5	57.0	723	3	AAY83227	Aay83227 PRO172 Po
9	527.5	57.0	723	3	AAB33422	

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:53:29 ; Search time 42 Seconds  
(without alignments)  
311.038 Million cell updates/sec

Title: US-09-783-931A-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	916	98.9	175	3	US-08-981-392-23	Sequence 23, Appl
2	916	98.9	175	4	US-09-908-322-23	Sequence 23, Appl
3	631.5	68.2	118	3	US-08-981-392-17	Sequence 17, Appl
4	631.5	68.2	118	4	US-09-908-322-17	Sequence 17, Appl
5	527.5	57.0	702	3	US-09-068-740A-4	Sequence 4, Appli
6	527.5	57.0	723	3	US-09-068-740A-9	Sequence 9, Appli
7	527.5	57.0	723	4	US-09-423-753-27	Sequence 27, Appl
8	527.5	57.0	723	4	US-09-641-612-6	Sequence 6, Appli
9	448	48.4	713	3	US-08-872-855-5	Sequence 5, Appli
10	428	46.2	720	3	US-08-872-855-4	Sequence 4, Appli
11	419	45.2	722	3	US-08-981-392-12	Sequence 12, Appl

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:56:20 ; Search time 164 Seconds  
(without alignments)  
412.844 Million cell updates/sec

Title: US-09-783-931A-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	916	98.9	175	9	US-09-908-322-23	Sequence 23, Appl
2	916	98.9	175	10	US-09-783-931-23	Sequence 23, Appl
3	631.5	68.2	118	9	US-09-908-322-17	Sequence 17, Appl
4	631.5	68.2	118	10	US-09-783-931-17	Sequence 17, Appl
5	527.5	57.0	702	9	US-09-995-593A-4	Sequence 4, Appli
6	527.5	57.0	702	20	US-11-051-631-4	Sequence 4, Appli
7	527.5	57.0	723	9	US-09-828-366-21	Sequence 21, Appl
8	527.5	57.0	723	9	US-09-995-593A-9	Sequence 9, Appli

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:50:15 ; Search time 40 Seconds  
(without alignments)  
420.948 Million cell updates/sec

Title: US-09-783-931A-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	428	46.2	722	2	I48324	DELTA-like 1 - mou	
2	388	41.9	728	2	I50719	C-Delta-1 - chicke	
3	126.5	13.7	685	2	JC7570	Delta-4 protein -	
4	125.5	13.6	686	2	JC7569	Delta-4 protein -	
5	88.5	9.6	1106	1	TVHUGL	transforming prote	
6	87.5	9.4	925	2	T29311	hypothetical prote	
7	86.5	9.3	504	2	T13475	hypothetical prote	
8	83.5	9.0	1651	2	T14160	transmembrane rece	
9	83	9.0	1707	2	T18951	hypothetical prote	
10	81	8.7	763	2	AC0108	probable primase Y	
11	79.5	8.6	326	2	A41732	heterogeneous ribo	
12	79.5	8.6	386	1	S22315	snRNP-associated p	
13	78.5	8.5	512	2	T47793	receptor-like prot	
14	77.5	8.4	538	2	T49418	hypothetical prote	

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:50:15 ; Search time 175 Seconds  
(without alignments)  
512.079 Million cell updates/sec

Title: US-09-783-931A-23  
Perfect score: 926  
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%				
No.	Score	Query Match	Length	DB	ID	Description
1	527.5	57.0	723	1	DLL1_HUMAN	O00548 homo sapien
2	445	48.1	714	1	DLL1_RAT	P97677 rattus norv
3	431	46.5	722	2	Q6PFV7	Q6pfv7 mus musculu
4	428	46.2	722	1	DLL1_MOUSE	Q61483 mus musculu
5	388	41.9	728	2	Q90656	Q90656 gallus gall
6	387.5	41.8	726	2	Q8AW87	Q8aw87 cynops pyrr
7	356	38.4	721	2	Q91902	Q91902 xenopus lae
8	294.5	31.8	717	2	P87357	P87357 brachydanio
9	294.5	31.8	720	2	Q8UWJ4	Q8uwj4 brachydanio
10	218	23.5	772	2	Q6DI48	Q6di48 brachydanio
11	149	16.1	802	2	O57462	O57462 brachydanio
12	126.5	13.7	685	1	DLL4_HUMAN	Q9nr61 homo sapien
13	126.5	13.7	686	1	DLL4_MOUSE	Q9ji71 mus musculu
14	125.5	13.6	686	2	Q9DBU9	Q9dbu9 mus musculu
15	91	9.8	364	2	Q6MZM8	Q6mzm8 homo sapien